

SMART; SM00320; WD40; 8.
 PROSITE; PS50896; LISH; 1.
 PROSITE; PS00678; WD REPEATS 1; 4.
 PROSITE; PS50082; WD REPEATS 2; 6.
 PROSITE; PS50294; WD_REPEATS_REGION; 1.
 Repeat; WD repeat.
 DOMAIN 4 36 LISH.
 REPEAT 167 206
 REPEAT 223 262
 REPEAT 264 303
 REPEAT 306 344
 REPEAT 347 386
 REPEAT 389 427
 REPEAT 440 479
 REPEAT 481 513
 REPEAT 518 559
 DOMAIN 108 118
 CONFLICT 31 31
 CONFLICT 59 59
 CONFLICT 389 389
 SEQUENCE 514 AA; 55595 MW; 0B556D2E4BA796D CRC64;
 Query Match 99.6%; Score 2716; DB 1; Length 514;
 Best Local Similarity 99.6%; Pred. No. 1.5e-188;
 Matches 512; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSISDEVNFLVYRLOESGFSHSAFTGKSHISQSNINGALVPPAALISIIKGLQVY 60
 1 MSISDEVNFLVYRLOESGFSHSAFTGKSHISQSNINGALVPPAALISIIKGLQVY 60
 61 EAIVSINEDGTLFDCRPTESLIDAVPVDVQVQYAYDKLQAAAAAASQ 120
 61 EAIVSINEDGTLFDCRPTESLIDAVPVDVQVQYAYDKLQAAAAAASQ 120
 121 QGSAKNGENTANGENGATIANHNTDMEVDGVEIPPNKAVVLRGHESEVFIQANPV 180
 121 QGSAKNGENTANGENGATIANHNTDMEVDGVEIPPNKAVVLRGHESEVFIQANPV 180
 181 SLLASGSDSTARIWNLSNSTSGTQVLRHCRIGGGQDVSNKDVTLSDWNSGTL 240
 181 SLLASGSDSTARIWNLSNSTSGTQVLRHCRIGGGQDVSNKDVTLSDWNSGTL 240
 241 ATGSDYDGFARITWDXGNLSTLQGHKGFIPALKWKNKGNFILSAGVDKTTIWDATG 300
 241 ATGSDYDGFARITWDXGNLSTLQGHKGFIPALKWKNKGNFILSAGVDKTTIWDATG 300
 301 KQOPFHPAPALDVQSNNTFASCTDMCHVCKLQGDRIKTFQGHTEVNAIKWDPT 360
 301 KQOPFHPAPALDVQSNNTFASCTDMCHVCKLQGDRIKTFQGHTEVNAIKWDPT 360
 361 GNLLASCSDDMTLKIWSKQDNVHDLQOHKEIYTIKWSPTGPTGNNPNANMLASAF 420
 361 GNLLASCSDDMTLKIWSKQDNVHDLQOHKEIYTIKWSPTGPTGNNPNANMLASAF 420
 421 DSTVLMDVDRGICHTLTKEQEPVSVASPDGRYLASGFKCVHIWNTQTGALVHSY 480
 421 DSTVLMDVDRGICHTLTKEQEPVSVASPDGRYLASGFKCVHIWNTQTGALVHSY 480
 481 RTGTGIFEVCAAGDKVYASGSDGVCVLDLRK 514
 481 RTGTGIFEVCAAGDKVYASGSDGVCVLDLRK 514

RESULT 2

TELEX HUMAN
 ID TELEX HUMAN STANDARD; PRT; 526 AA.
 AC O60907;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 RE Transducin beta-like 1X protein (Transducin-beta-like 1, X-linked).
 RE TELEX OR TELI.
 RE Homo sapiens (Human).
 RE Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9264241; PubMed=10330347;
 RA Bassi M.T., Ramesar R.S., Caciotti B., Winship I.M., De Grandi A.,
 RA Riboni M., Townes P.L., Beighton P., Ballabio A., Borsani G.,
 RT "X-linked late-onset sensorineural deafness caused by a deletion
 RL involving OAI and a novel gene containing WD-40 repeats.",
 RN Am. J. Hum. Genet. 64:1604-1616(1999).
 RP [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellaro N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- TISSUE SPECIFICITY: Ubiquitous.
 CC -!- SIMILARITY: Contains 1 Lish domain.
 CC -!- SIMILARITY: Contains 8 WD repeats.
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 DR EMBL; Y12781; CAA73319.1; ALT_INIT.
 DR EMBL; BC032708; AAH32708.1; -.
 DR Genbank; HGNC:11585; TBL1X.
 DR MIM; 300196; -.
 DR GO; GO:0007605; P:heating; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR GO; GO:0007601; P:vision; TAS.
 DR InterPro; IPR006594; LISH.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; WD40; 8.
 DR PRINTS; PR00320; GPROTEINRPT.
 DR ProDom; PD000018; WD40; 3.
 DR SMART; SM00667; Lish; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS50896; LISH; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 4.
 DR PROSITE; PS50082; WD_REPEATS_2; 6.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 FT DOMAIN 4 36 LISH.
 FT REPEAT 179 218 WD 1.
 FT REPEAT 235 274 WD 2.
 FT REPEAT 276 315 WD 3.
 FT REPEAT 318 358 WD 4.
 FT REPEAT 359 398 WD 5.
 FT REPEAT 401 449 WD 6.
 FT REPEAT 452 491 WD 7.

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FT REPEAT 493 525 WD 8.
FT DOMAIN 108 124 POLY.ALA.
SO SEQUENCE 526 AA; 57048 MW; 98922F88BC42F639 CRC64;

Query Match 89.4%; Score 2437; DB 1; Length 526;
Best Local Similarity 86.0%; Pred. No. 2.1e-168;
Matches 453; Conservative 33; Mismatches 27; Indels 14; Gaps 2;

QY 1 MSISDEVNLFVYLOESGSHAFTEGKSHISQSNINGALVPPAALISIIQKGLQYV 60
DQ 1 MSISDEVNLFVYLOESGSHAFTEGKSHISQSNINGALVPPAALISIIQKGLQYV 60
QY 61 EAEVSIINEDGTLFDRPIESLSLDVAMPDVVQTRQOAYRDKLAQQOAAAAA--- 117
DQ 61 EAEVSIINEDGTLFDRPIESLSLDVAMPDVVQTRQOAYRDKLAQQOAAAAAATAA 120
QY 118 -----ASQGSXKNGENTANGENGAAHTIANNHTDMVEVDGVEIPPNKAVVLRG 167
DQ 121 ATAATTTAGVSHQNPCKNREATVNGENRAHSV-NNHAKPMEIDGVEIPSSKATVLRG 179
QY 168 HESVFTICANVPVSDLLASGSDSTARIWNLSNSTSGTOLVLRHCIREGGODVPSNKD 227
DQ 180 HESVFTICANVPVSDLLASGSDSTARIWNLSNSTSGTOLVLRHCIREGGHDVPSNKD 239
QY 228 VTSLDWNSGTLATSYDGFARITWKDGNLSTLQGHKGPITFALKWNKNGNFIISAGVD 287
DQ 240 VTSLDWNTGTLATSYDGFARITWKDGNLSTLQGHKGPITFALKWNKNGNFIISAGVD 299
QY 288 KTIINWDAHTGEAKQOFPFHSAPALDVWDQSNNTFASCSTDMCIHVCKLQCDRPIKTFQG 347
DQ 300 KTIINWDAHTGEAKQOFPFHSAPALDVWDQSNNTFASCSTDMCIHVCKLQCDRPIKTFQG 359
QY 348 HTNEVNAIKWDPKTMILLASCSDDMTLKIWSKODNCVHDIQHNKEIYTIKWSPTGPGTN 407
DQ 360 HTNEVNAIKWDPKTMILLASCSDDMTLKIWSKODNCVHDIQHNKEIYTIKWSPTGPGTN 419
QY 408 NPANMLASASFDSTVRLMDVGRGICHTLTKHQEPVYVAFSPDGRYLAGSFDKCVH 467
DQ 420 NPANMLASASFDSTVRLMDVGRGICHTLTKHQEPVYVAFSPDGRYLAGSFDKCVH 479
QY 468 IWNTOCALVHSYRGVGTGGEFEVCNNAAGDKVGSASDGSVCVLDLRK 514
DQ 480 IWNTOCALVHSYRGVGTGGEFEVCNNAAGDKVGSASDGSVCVLDLRK 526

RESULT 3
TBLY HUMAN
ID TBLY HUMAN STANDARD; PRT; 522 AA.
AC Q8BQ87;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transducin beta-like 1 protein (Transducin-beta-like 1, y-linked).
GN TBLY OR TBLY.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kuroda-Kawaguchi T., Skaletsky H., Minx P.J., Brown L.G., Rozen S.,
RA Wilson R.K., Waterston R.H., Page D.C.;
RT "The DNA sequence of the human y chromosome.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 Lish domain.
CC -1- SIMILARITY: Contains 8 WD repeats.
CC -----
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CC EMBL; AF332220; AAK13472.1; -
CC EMBL; AF332221; AAK13473.1; -
DR EMBL; AF332222; AAK13474.1; -
DR Genew; HGNC:18502; TBLY.
DR InterPro; IPR006594; Lish.
DR InterPro; IPR001690; WD40.
DR Pfam; PF00400; WD40; 8.
DR PRINTS; PRO3320; GPROTEINBRPT.
DR ProDom; PD000018; WD40; 3.
DR SMART; SM00667; Lish; 1.
DR SMART; SM00320; WD40; 8.
DR PROSITE; PS00896; Lish; 1.
DR PROSITE; PS00678; WD REPEATS 1; 4.
DR PROSITE; PS00882; WD REPEATS 2; 6.
DR PROSITE; PS00294; WD REPEATS REGION; 1.
KW Repeat; WD repeat.
FT DOMAIN 4 36 LISH.
FT REPEAT 177 216 WD 1.
FT REPEAT 233 272 WD 2.
FT REPEAT 274 313 WD 3.
FT REPEAT 316 354 WD 4.
FT REPEAT 357 396 WD 5.
FT REPEAT 399 447 WD 6.
FT REPEAT 450 489 WD 7.
FT REPEAT 491 521 WD 8.
SQ SEQUENCE 522 AA; 56688 MW; 4E020216422442D8 CRC64;

Query Match 86.8%; Score 2367; DB 1; Length 522;
Best Local Similarity 84.5%; Pred. No. 2.4e-163;
Matches 442; Conservative 35; Mismatches 34; Indels 12; Gaps 2;

QY 1 MSISDEVNLFVYLOESGSHAFTEGKSHISQSNINGALVPPAALISIIQKGLQYV 60
DQ 1 MSISDEVNLFVYLOESGSHAFTEGKSHISQSNINGALVPPAALISIIQKGLQYV 60
QY 61 EAEVSIINEDGTLFDRPIESLSLDVAMPDVVQTRQOAYRDKLAQQOAAAAA--- 115
DQ 61 EAEVSIINEDGTLFDRPIESLSLDVAMPDVVQTRQOAYRDKLAQQOAAAAAATAA 120
QY 116 -----AAASQGSXKNGENTANGENGAAHTIANNHTDMVEVDGVEIPPNKAVVLRGHE 169
DQ 121 AATMTAAISQNPCKNREATVNGENGAHEI-NNHAKPMEIDGVEIPPNKATVLRGHE 179
QY 170 SEVFTICANVPVSDLLASGSDSTARIWNLSNSTSGTOLVLRHCIREGGODVPSNKDVT 229
DQ 180 SEVFTICANVPVSDLLASGSDSTARIWNLSNSTSGTOLVLRHCIREGGHDVPSNKDVT 239
QY 230 SLDWNSGTLATSYDGFARITWKDGNLSTLQGHKGPITFALKWNKNGNFIISAGVDKT 289
DQ 240 SLDWNSGTLATSYDGFARITWKDGNLSTLQGHKGPITFALKWNKNGNFIISAGVDKT 299
QY 290 TIIWDAHTGEAKQOFPFHSAPALDVWDQSNNTFASCSTDMCIHVCKLQCDRPIKTFQGHT 349
DQ 300 TIIWDAHTGEAKQOFPFHSAPALDVWDQSNNTFASCSTDMCIHVCKLQCDRPIKTFQGHT 359
QY 350 NEVNAIKWDPKTMILLASCSDDMTLKIWSKODNCVHDIQHNKEIYTIKWSPTGPGTN 409
DQ 360 NEVNAIKWDPKTMILLASCSDDMTLKIWSKODNCVHDIQHNKEIYTIKWSPTGPGTN 419
QY 410 NANMLASASFDSTVRLMDVGRGICHTLTKHQEPVYVAFSPDGRYLAGSFDKCVH 469
DQ 420 NSSMLASASFDSTVRLMDVGRGICHTLTKHQEPVYVAFSPDGRYLAGSFDKCVH 479
QY 470 NTOTCALVHSYRGVGTGGEFEVCNNAAGDKVGSASDGSVCVLDLRK 512
DQ 480 NTOTCALVHSYRGVGTGGEFEVCNNAAGDKVGSASDGSVCVLDLRK 522

RESULT 4
TBLY MOUSE
ID TBLY_MOUSE STANDARD; PRT; 313 AA.

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